Attachment to Paper No 30

Form 1449 (Modified) **Information Disclosure Statement By Applicant** (Use Several Sheets if Necessary)	Atty Docket No. MXGNP002X1 Applicant: Selifonov et al. Filing Date February 1, 2000	Application No.: 09/495,668 Group 1637

U.S. Patent Documents

Examiner Initial	No.	Patent No.	Date	Patentee	Class	Sub-class	Filing Date
	A1						
	A2						
	A3						
	A4						
	A5						
	A6						
	A7						
	A8						

Foreign Patent or Published Foreign Patent Application

Examiner Initial	No.	Document No.	Publication Date	Country or Patent Office	Class	Sub-class	Translation Yes	Translation No
	B1							
	B2							
	B3							
	B4							
	B5							

Other Documents

Examiner Initial	No.	Author, Title, Date, Place (e.g. Journal) of Publication
	C1	Moore et al., *Modeling and Optimization of DNA Recombination,* Computer and Chemical Engineering 2000, Department of Chemical Engineering, The Pennsylvania State University, University Park © 2000
	C2	Gregory L. Moore, Costas D. Maranas, *Modeling DNA Mutation and Recombination for Directed Evolution Experiments,* Department of Chemical Engineering, The Pennsylvania State University, University Park, Received 28, October 1999, Accepted in revised form 15 April 2000 © 2000 Academic Press

Examiner	Date Considered
	1-6-03.

Examiner: Initial citation considered. Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

Attachment to Paper No 2

Form 1449 (Modified) **Information Disclosure Statement By Applicant** (Use Several Sheets if Necessary)	Atty Docket No. MXGNP002X1/0159.210 Applicant: Selifonov et al. Filing Date February 1, 2000	Application No.: 09/495,668 Group 1631

U.S. Patent Documents

Examiner Initial	No.	Patent No.	Date	Patentee	Class	Sub-class	Filing Date
	A1	6,125,331	9/26/00	Toh			
	A2	6,403,312	6/11/02	Dahiyat, et al			
	A3	6,455,254	9/24/02	Short			

Foreign Patent or Published Foreign Patent Application

Examiner Initial	No.	Document No.	Publication Date	Country or Patent Office	Class	Sub-class	Translation Yes	Translation No
	B1	WO00/47612	8/17/00	WIPO				
	B2	WO01/61344	8/23/01	WIPO				
	B3	WO00/42559	7/2/00	WIPO				
	B4	WO01/75767	10/11/01	WIPO				

Other Documents

Examiner Initial	No.	Author, Title, Date, Place (e.g. Journal) of Publication
	C1	Young et al., "Characterization of Receptor Binding Determinants of Granulocyte Colony Stimulating Factor," *Protein Science* 6:1228-1236, 1997
	C2	Dahiyat and Mayo, "Protein Design Automation," Protein Science, 5:895-903, (1996)
	C3	Su et al., "Coupling Backbone Flexibility and Amino Acid Sequence Selection in Protein Design," Protein Science, 6:1701-1707, (1997)
	C4	Voigt et al., "Computationally Focusing the Directed Evolution of Proteins," Journal of Cellular Biochemistry Supplement, 37:58-63 (2001)
	C5	Hellberg et al., "Minimum Analogue Peptide Sets (MAPS) for quantitative Structure-Activity Relationships," Int. J. Peptide Protein Res. 37:414-427 (1991)

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(Use Several Sheets if Necessary)	Filing Date February 1, 2000	Group 1631

	C6	Martin van Heel, "A New Family of Powerful Multivariates Statistical Sequence Analysis Techniques," J. Mol. Biol, 220:877-887 (1991)
	C7	Goldman et al., "Estimating Protein Function From Combinatorial Sequence Data Using Decision Algorithms and Neural Networks," Drug Dev. Research 33:125-132 (1994)
	C8	Gustafsson et al., "Exploration of Sequence Space for Protein Engineering," J. Mol. Recognit. 14:308-314 (2001)
	C9	Miyazawa et al., "Residue-Residue Potentials with a Favorable Contact Pair Term and an Unfavorable High Packing Density Term, for Simulation and Threading," J. Mol. Biol., 256:623-644 (1996)
	C10	Chao Zhang, "Extracting Contact Energies From Protein Structures: A Study Using a Simplified Model," Proteins: Structure, Function, and Genetics, 31:299-308 (1998)
	C11	Miyazawa et al., "Self-Consistent Estimation of Inter-Residue Protein Contact Engergies Based on an Equilibrium Mixture Approximation of Residues," Proteins: Structure, Function, and Genetics, 34:49-68 (1999)
	C12	Miyazawa et al., "An Empirical Energy Potential With a References State for Protein Fold and Sequence Recognition," Proteins: Structure, Function, and Genetics, 36:357-369 (1999)
	C13	Moore et al., "Predicting Crossover Generation in DNS Shuffling," PNAS, Vol. 98, No. 6, 3226-3231 (2001)
	C14	Lehman et al., "Engineering Proteins for Thermostability: the Use of Sequence Alignments Versus Rational Design and Directed Evolution," Current Opinion in Biotechnology, 13:371-375 (2001)
	C15	Colleen Kelly, "A Test of the Markovian Model of DNA Evolution," Biometrics 50, 653-664, (1994)
	C16	H.W. Hellinga, "Rational Protein Design: Combining Theory and Experiment," Proc. Natl. Acad. Sci. USA, Vol. 94, pp. 10015-10017, (1997)
	C17	William F. DeGrado, "Proteins from Scratch," Science, Vol. 278, 80-81 (1997)

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	C18	Jonsson, et al, "Quaintitative Sequence-Activity Modeils (QSAM)- Tool For Sequence Design", Nuclear Acid Research Vol. 21, No. 3, pp. 733-739 (1993)
	C19	Sjostrom, et al, "Signal Peptide Amino Acid Sequences In *Escheruchua coli* Contain Information Related To Final Protein Localization. A Multivariate Data Analysis", The CMBO Journal vol. 6, no. 3, pp 823-831, (1987)
	C20	Patel, et al, "Patenting Computer-Designed Peptides", Journal Of Computer-Acid Molecular Design 12 pp543-556, (1998)
	C21	Schneider, et al, "Peptide Design by Artificial Neural Networks and Computer-Based Evolutionary Search", Proc. Natl. Acad. Sci. USA, vol. 95, pp. 12179-121184, October 1998
	C22	Mee, et al, "Design of Active Analogues of a 15-Residue Peptide Using D-Optimal Design QSAR and a Combinatorial Search Algorithm", J Peptide Res. 49, pp. 89-102, (1997)
	C23	Bogarad, et al, "A Hierarchical Approach to Protein Molecular Evolution", Proc. Natl. Acad. Sci. USA, Vol. 96, pp. 2597-2595, March 1999
	C24	Darius, et al, "Simulated Molecular Evolution" Or Computer-Generated Artifacts?", Biophysical Journal, Vol. 67, pp. 2120-2122, November 1994
Examiner		Date Considered 1-6-03

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